1645

ENTERED

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           RAW SEQUENCE LISTING              DATE: 05/19/2000
           PATENT APPLICATION:  US/09/201,916A    TIME: 12:37:02

           Input Set : A:\DYOU17.001AUS.TXT
           Output Set: N:\CRF3\05182000\I201916A.raw
```

```
 4 <110> APPLICANT: Hope, Ralph Graham
 5        Mclauchlan, John
 7 <120> TITLE OF INVENTION: VIRAL THERAPEUTICS
10 <130> FILE REFERENCE: DYOU17.001AUS
12 <140> CURRENT APPLICATION NUMBER: 09/201916A
13 <141> CURRENT FILING DATE: 1998-12-01
15 <160> NUMBER OF SEQ ID NOS: 13
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 630
21 <212> TYPE: DNA
22 <213> ORGANISM: Hepatitis C Virus
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (43)...(630)
28 <400> SEQUENCE: 1
29 ggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca cc atg agc acg aat       54
30                                                  Met Ser Thr Asn
31                                                   1
33 cct aaa cct caa aga aaa acc aaa cgt aac acc aac cgt cgc cca cag      102
34 Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln
35   5              10                  15                  20
37 gac gtt aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt tac ttg     150
38 Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu
39                  25                  30                  35
41 ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg acg agg aag act     198
42 Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr
43                  40                  45                  50
45 tcc gag cgg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gca     246
46 Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala
47              55                  60                  65
49 cgt cgg ccc aag ggc agg aac tgg gct cag ccc ggg tat cct tgg ccc     294
50 Arg Arg Pro Lys Gly Arg Asn Trp Ala Gln Pro Gly Tyr Pro Trp Pro
51       70                  75                  80
53 ctc tat ggc aat gag ggt tgc ggg tgg gcg gga tgg ctc ctg tcc ccc     342
54 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro
55   85                  90                  95                 100
57 agt ggc tct cgg cct agt tgg ggc ccc aac gac ccc cga cgt agg tcg     390
58 Ser Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro Arg Arg Arg Ser
59                 105                 110                 115
61 cgc aat ttg ggt aag gtc atc gat acc ctt acg tgc ggc ttc gtc gat     438
62 Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Val Asp
63                 120                 125                 130
65 ctc atg ggg tac ata ccg ctc gtc ggc gcc cct ctt aga ggc gct gcc     486
66 Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Arg Gly Ala Ala
67                 135                 140                 145
69 agg gcc ctg gcg cat ggc gtc cgg gtt ctg gaa gac ggt gtg aac tat     534
```

RAW SEQUENCE LISTING   DATE: 05/19/2000
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    Input Set : A:\DYOU17.001AUS.TXT
    Output Set: N:\CRF3\05182000\I201916A.raw

```
70 Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr
71     150                 155                 160
73 gca aca ggt aac ctt cct ggt tgc tct ttc tct atc ttc ctt ctg gcc      582
74 Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala
75 165                 170                 175                 180
77 ctg ctc tct tgc ctg act gtg ccc gct tca gcc tac caa gtg cgc aac      630
78 Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
79                 185                 190                 195
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 60
84 <212> TYPE: DNA
85 <213> ORGANISM: Hepatitis C Virus
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (1)...(60)
90 <223> OTHER INFORMATION: Corresponds to aa 125 to 144 of SEQ ID. No. 1
92 <400> SEQUENCE: 2
93 acc ctt acg tgc ggc ttc gtc gat ctc atg ggg tac ata ccg ctc gtc      48
94 Thr Leu Thr Cys Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val
95 1               5                   10                  15
97 ggc gcc cct ctt                                                      60
98 Gly Ala Pro Leu
99             20
102 <210> SEQ ID NO: 3
103 <211> LENGTH: 18
104 <212> TYPE: DNA
105 <213> ORGANISM: Hepatitis C Virus
107 <220> FEATURE:
108 <221> NAME/KEY: CDS
109 <222> LOCATION: (1)...(18)
110 <223> OTHER INFORMATION: Corresponds to aa 161-166 of SEQ ID. No. 1
112 <400> SEQUENCE: 3
113 ggt gtg aac tat gca aca                                             18
114 Gly Val Asn Tyr Ala Thr
115 1               5
118 <210> SEQ ID NO: 4
119 <211> LENGTH: 1900
120 <212> TYPE: DNA
121 <213> ORGANISM: Human
123 <220> FEATURE:
124 <221> NAME/KEY: misc_feature
125 <222> LOCATION: (1)...(1900)
126 <223> OTHER INFORMATION: n = A,T,C or G
128 <400> SEQUENCE: 4
129 cgtcttcggg acgcgcccgc tcttcgcctt tcgctgcagt ccgtcgattt ctttctccag      60
130 gaagaaaaat ggcatccgtt gcagttgatc cacaaccgag tgtggtgact cgggtggtca     120
131 acctgccctt ggtgagctcc acgtatgacc tcatgtcctc agcctatctc agtacaaagg     180
132 accagtatcc ctacctgaag tctgtgtgtg agatgscaga gaacggtgtg aagaccatca     240
133 cctccgtggc catgaccagt gctctgccca tcatccagaa gctagagccg caaattgcag     300
```

```
      134 ttgccgatac ctatgcctgt aaggggctag acaggattga ggagagactg cctattctga    360
      135 atcagccatc aactcagatt gttgccaatg ccaaaggcgc tgtgactggg gcaaaagatg    420
W--> 136 ctgtgacgac tactgtgact ggggccaagg attctgtngc cagcacgatc acaggggtga    480
      137 tggacaagac caaaggggca gtgactggca gtgtgagaa gaccaagtct gtggtcagtg    540
      138 gcagcattaa cacagtcttg gggagtcgga tgatgcagct cgtgagcagt ggcgtagaaa    600
      139 atgcactcac caaatcagag ctgttggtag aacagtacct ccctctcact gaggaagaac    660
      140 tagaaaaaga agcaaaaaaa gttgaaggat ttgatctggt tcagaagcca agttattatg    720
      141 ttagactggg atccctgtct accaagcttc actcccgtgc ctaccagcag gctctcagca    780
      142 gggttaaaga agctaagcaa aaaagccaac agaccatttc tcagctccat tctactgttc    840
      143 acctgattga atttgccagg aagaatgtgt atagtgccaa tcagaaaatt caggatgctc    900
      144 aggataagct ctacctctca tgggtagagt ggaaaaggag cattggatat gatgatactg    960
      145 atgagtccca ctgtgctgag cacattgagt cacgtactct tgcaattgcc cgcaacctga   1020
      146 ctcagcagct ccagaccacg tgccacaccc tcctgtccaa catccaaggt gtaccacaga   1080
      147 acatccaaga tcaagccaag cacatggggg tgatggcagg cgacatctac tcagtgttcc   1140
      148 gcaatgctgc ctccttaaa gaagtgtctg acagcctcct cacttctagc aagggcagc   1200
      149 tgcagaaaat gaaggaatct ttagatgacg tgatggatta tcttgttaac aacacgcccc   1260
      150 tcaactggct ggtaggtccc ttttatcctc agctgactga gtctcagaat gctcaggacc   1320
      151 aaggtgcaga gatggacaag agcagccagg agacccagcg atctgagcat aaaactcatt   1380
      152 aaacctgccc ctatcactag tgcatgctgt ggccagacag atgacacctt ttgttatgtt   1440
      153 gaaattaact tgctaggcaa ccctaaattg ggaagcaagt agctagtata aaggccctca   1500
      154 attgtagttg tttccagctg aattaagagc tttaaagttt ctggcattag cagatgattt   1560
      155 ctgttcacct ggtaagaaaa gaatgatagg cttgtcagag cctatagcca gaactcagaa   1620
      156 aaaattcaaa tgcacttatg ttctcattct atggccattg tgttgcctct gttactgttt   1680
      157 gtattgaata aaaacatctt catgtgggct ggggtagaaa ctggtgtctg ctctggtgtg   1740
      158 atctgaaaag gcgtcttcac tgctttatct catgatgctt gcttgtaaaa cttgatttta   1800
      159 gtttttcatt tctcaaatag gaatactacc tttgaattca ataaaattca ctgcaggata   1860
W--> 160 gaccagttna gnagcaaaca nncangtaca cnnaaganac                          1900
      162 <210> SEQ ID NO: 5
      163 <211> LENGTH: 437
      164 <212> TYPE: PRT
      165 <213> ORGANISM: Human
      167 <220> FEATURE:
      168 <221> NAME/KEY: VARIANT
      169 <222> LOCATION: (1)...(437)
      170 <223> OTHER INFORMATION: Xaa = Any Amino Acid
      172 <400> SEQUENCE: 5
      173 Met Ala Ser Val Ala Val Asp Pro Gln Pro Ser Val Val Thr Arg Val
      174 1               5                   10                  15
      175 Val Asn Leu Pro Leu Val Ser Ser Thr Tyr Asp Leu Met Ser Ser Ala
      176             20                  25                  30
      177 Tyr Leu Ser Thr Lys Asp Gln Tyr Pro Tyr Leu Lys Ser Val Cys Glu
      178             35                  40                  45
W--> 179 Met Xaa Glu Asn Gly Val Lys Thr Ile Thr Ser Val Ala Met Thr Ser
      180     50                  55                  60
      181 Ala Leu Pro Ile Ile Gln Lys Leu Glu Pro Gln Ile Ala Val Ala Asp
      182 65                  70                  75                  80
      183 Thr Tyr Ala Cys Lys Gly Leu Asp Arg Ile Glu Glu Arg Leu Pro Ile
      184             85                  90                  95
      185 Leu Asn Gln Pro Ser Thr Gln Ile Val Ala Asn Ala Lys Gly Ala Val
```

RAW SEQUENCE LISTING   DATE: 05/19/2000
PATENT APPLICATION: US/09/201,916A   TIME: 12:37:02

Input Set : A:\DYOU17.001AUS.TXT
Output Set: N:\CRF3\05182000\I201916A.raw

```
186              100              105              110
187 Thr Gly Ala Lys Asp Ala Val Thr Thr Thr Val Thr Gly Ala Lys Asp
188         115              120              125
189 Ser Val Ala Ser Thr Ile Thr Gly Val Met Asp Lys Thr Lys Gly Ala
190     130              135              140
191 Val Thr Gly Ser Val Glu Lys Thr Lys Ser Val Val Ser Gly Ser Ile
192 145              150              155              160
193 Asn Thr Val Leu Gly Ser Arg Met Met Gln Leu Val Ser Ser Gly Val
194             165              170              175
195 Glu Asn Ala Leu Thr Lys Ser Glu Leu Leu Val Glu Gln Tyr Leu Pro
196             180              185              190
197 Leu Thr Glu Glu Glu Leu Glu Lys Glu Ala Lys Lys Val Glu Gly Phe
198         195              200              205
199 Asp Leu Val Gln Lys Pro Ser Tyr Tyr Val Arg Leu Gly Ser Leu Ser
200     210              215              220
201 Thr Lys Leu His Ser Arg Ala Tyr Gln Gln Ala Leu Ser Arg Val Lys
202 225              230              235              240
203 Glu Ala Lys Gln Lys Ser Gln Gln Thr Ile Ser Gln Leu His Ser Thr
204             245              250              255
205 Val His Leu Ile Glu Phe Ala Arg Lys Asn Val Tyr Ser Ala Asn Gln
206             260              265              270
207 Lys Ile Gln Asp Ala Gln Asp Lys Leu Tyr Leu Ser Trp Val Glu Trp
208         275              280              285
209 Lys Arg Ser Ile Gly Tyr Asp Asp Thr Asp Glu Ser His Cys Ala Glu
210     290              295              300
211 His Ile Glu Ser Arg Thr Leu Ala Ile Ala Arg Asn Leu Thr Gln Gln
212 305              310              315              320
213 Leu Gln Thr Thr Cys His Thr Leu Leu Ser Asn Ile Gln Gly Val Pro
214             325              330              335
215 Gln Asn Ile Gln Asp Gln Ala Lys His Met Gly Val Met Ala Gly Asp
216         340              345              350
217 Ile Tyr Ser Val Phe Arg Asn Ala Ala Ser Phe Lys Glu Val Ser Asp
218         355              360              365
219 Ser Leu Leu Thr Ser Ser Lys Gly Gln Leu Gln Lys Met Lys Glu Ser
220     370              375              380
221 Leu Asp Asp Val Met Asp Tyr Leu Val Asn Asn Thr Pro Leu Asn Trp
222 385              390              395              400
223 Leu Val Gly Pro Phe Tyr Pro Gln Leu Thr Glu Ser Gln Asn Ala Gln
224             405              410              415
225 Asp Gln Gly Ala Glu Met Asp Lys Ser Ser Gln Glu Thr Gln Arg Ser
226         420              425              430
227 Glu His Lys Thr His
228         435
230 <210> SEQ ID NO: 6
231 <211> LENGTH: 31
232 <212> TYPE: PRT
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: A branched peptide containing residues 5-27 of the
```

RAW SEQUENCE LISTING   DATE: 05/19/2000
PATENT APPLICATION: US/09/201,916A   TIME: 12:37:02

Input Set : A:\DYOU17.001AUS.TXT
Output Set: N:\CRF3\05182000\I201916A.raw

```
237      HCV core protein.
239 <221> NAME/KEY: VARIANT
240 <222> LOCATION: (1)...(31)
241 <223> OTHER INFORMATION: Xaa = Ala or Pro at position 1, and Ile or Asn at
242       postion 12.
244 <400> SEQUENCE: 6
245 Xaa Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Xaa Arg Arg Pro Gln
246 1               5                  10                  15
247 Asp Val Lys Phe Pro Gly Gly Lys Lys Lys Lys Lys Lys Ala
248             20                  25                  30
250 <210> SEQ ID NO: 7
251 <211> LENGTH: 11
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
257       protein deletion plasmids.
259 <400> SEQUENCE: 7
260 gctgagatct a                                                    11
262 <210> SEQ ID NO: 8
263 <211> LENGTH: 29
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
269       protein deletion plasmids.
271 <400> SEQUENCE: 8
272 gtaaccttcc tggttgctct tgagatcta                                 29
274 <210> SEQ ID NO: 9
275 <211> LENGTH: 17
276 <212> TYPE: DNA
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
281       protein deletion plasmids.
283 <400> SEQUENCE: 9
284 gtaacctttg agatcta                                              17
286 <210> SEQ ID NO: 10
287 <211> LENGTH: 18
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
293       protein deletion plasmids.
295 <400> SEQUENCE: 10
296 ctggcgcatt gagatcta                                             18
298 <210> SEQ ID NO: 11
299 <211> LENGTH: 28
300 <212> TYPE: DNA
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VERIFICATION SUMMARY   DATE: 05/19/2000
PATENT APPLICATION: US/09/201,916A   TIME: 12:37:03

Input Set : A:\DYOU17.001AUS.TXT
Output Set: N:\CRF3\05182000\I201916A.raw

```
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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